Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-3 (canceled)

4. (currently amended) The method ~~as in claims 32 or~~ of claim 33 comprising an additional step of cleaving the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules into fragments, prior to the step of examining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

5. (Currently amended) The method ~~as in claims 32 or~~ of claim 33 comprising an additional step of denaturing the molecules prior to step (ii).

6. (currently amended) The method ~~as in claims 32 or~~ of claim 33 wherein the step of examining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry comprises introducing the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules to a mass spectrometer using electrospray ionization.

7. (previously presented) The method of claim 6 wherein the electrospray ionization method is selected from the group consisting of nanospray, pneumatically assisted electrospray, ionspray and turboionspray.

8. (currently amended) The method ~~as in claims 32 or~~ of claim 33 comprising an additional step of separating the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules into sub-fractions before the step of examining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

9. (currently amended) The method of claim 8 wherein the step of separating the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules uses a separator selected from the group consisting of 1-D gel electrophoresis, SDS-PAGE, isoelectric focusing, 2-D gel electrophoresis, zone electrophoresis, isotachophoresis, ion exchange chromatography, normal phase chromatography, reverse phase chromatography,

hydrophobic interaction chromatography, size exclusion chromatography and any combination of these separators.

10. (currently amended) The method of claim 4 comprising an additional step of separating the fragments after the step of cleaving the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules and before the step of examining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules.

11. (previously presented)The method of claim 10 wherein the step of separating the fragments uses a separator selected from the group consisting of liquid chromatography, high performance liquid chromatography and capillary electrophoresis.

12. (currently amended) The method ~~as in claims 32 or~~ of claim 33 comprising an additional step of analyzing the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules after the step of examining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

13. (currently amended) The method of claim 12 wherein the derivatives are peptides and the step of analyzing the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules is selected from the group consisting of collision-induced dissociation in a mass spectrometer operating in MS/MS mode, peptide mass fingerprinting, peptide mapping, Edman sequencing and sequencing by sequential amino acid cleavage.

14. (currently amended) The method of claim 13, comprising an additional step of sequencing the molecules, after the step of analyzing the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules.

15. (canceled)

16. (canceled)

17. (Currently amended) The method ~~as in claims 32 or~~ of claim 33 wherein the reducing agent is selected from the group consisting of a sodium cyanoborohydride, sodium borohydride, dialkyl borane complexes and pyridine borane complexes.

18. (Currently amended) The method ~~as in claims 32 or~~ of claim 33 wherein the molecules are selected from the group consisting of cells, cellular extracts, sub-cellular extracts, cellular lysates, peptides, proteins, drugs, toxins, antibodies and pollutants.

19. (previously presented) The method of claim 18 wherein the sample comprises a protein having an amine and the protein is extracted from a cell.

20. (previously presented) The method of claim 19 wherein the amine of the protein is selected from the group consisting of a lysine residue, ornithine residue and a residue at the N- terminal amino group of the protein.

21. (currently amended) The method ~~as in claims 32 or~~ of claim 33 wherein the step of examining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry utilizes a mass spectrometer selected from the group consisting of:

(i) Fourier transform – Ion cyclotron resonance mass spectrometers (FT-ICR-MS);

(ii) Time of Flight mass spectrometers (TOF-MS, TOF-TOF-MS);

(iii) Ion trap mass spectrometers (IT);

(iv) Quadrupole mass spectrometers (Q-MS and QqQ-MS);

(v) Ion mobility mass spectrometers (IM-MS);

(vi) Quadrupole (or hexapole, octapole)-Time of Flight mass spectrometers (Q-TOF, and Qq-TOF); and

(vii) Ion trap – Time of flight mass spectrometers (IT-TOF).

22. (previously presented) The method of claim 21 comprising an additional step of combining the mass spectrometer with an ionization source.

23 (previously presented) The method of claim 22 wherein the ionization source is selected from the group consisting of electrospray ionization, matrix-assisted laser desorption and ionization (MALDI), field desorption, thermal desorption and laser desorption.

Claims 24-32 (canceled)

33. (currently amended) A method for the simultaneous quantitative analysis of ~~up~~ 3 to 8 samples comprising molecules, wherein each of the molecules has an amine bearing an active hydrogen, the method comprising:

(i) providing ~~up to 8 combinations~~ one combination of differential isotope labelled reagents for each of the samples, wherein each combination contains a reducing agent and an aldehyde selected from formaldehyde and acetaldehyde ~~and a reducing agent~~, and each of the ~~up to 8~~ combinations of differential isotope reagents is isotopically distinct from each other;

(ii) reacting each of the samples ~~comprising molecules~~ with one of the ~~one of the up to 8~~ combinations of reagents, wherein the reacting results in a reductive alkylation of the amine of the molecules to alkylamine derivatives of the molecules, to provide ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules that are differentially isotope labelled from each other at an alkylamine;

(iii) combining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of the molecules for examination by mass spectrometry; and

(iv) examining the ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules by mass spectrometry.

34. (currently amended) A preparation for simultaneous quantitative analysis by mass spectrometry, the preparation comprising ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules, said derivatives labelled from each other at an alkylamine ~~each of the up to 8 samples of differential isotope labelled derivatives of molecules~~ resulting from a reductive alkylation of an amine reaction of (a) 3 to 8 samples of molecules having an amine bearing an active hydrogen with (b) a combination of differential isotope labelled reagents for each of the samples, wherein each combination contains a reducing agent and an aldehyde selected from formaldehyde ~~and a reducing agent~~, and each ~~the~~ combination of differential isotope labelled reagents is isotopically distinct from each other. ~~with (b) a sample of molecules.~~

35. (Canceled)

36. (currently amended) A method for the quantitative analysis of ~~up~~ 3 to 8 samples of cellular extracts, each of the ~~up~~ 3 to 8 samples of cellular extracts comprising molecules having an amine bearing an active hydrogen, the method comprising:

(i) providing ~~up to 8 combinations~~ one combination of differential isotope labelled reagents for each of the samples, wherein each combination contains a reducing agent and an aldehyde selected from formaldehyde and acetaldehyde ~~and a reducing agent~~, and each of the ~~up to 8~~ combinations of differential isotope reagents is isotopically distinct from each other;

(ii) reacting each sample with one of the combinations of differential isotope labelled reagents to produce ~~up~~ 3 to 8 samples of differential isotope labelled derivatives of molecules, wherein the reacting results in a reductive alkylation of the amine of the molecules to alkylamine derivatives of the molecules, such that the ~~up~~ 3 to 8 samples of differential labelled derivatives of molecules are differentially isotope labelled from each other at an alkylamine;

(iii) combining the ~~up~~ 3 to 8 samples of differential labelled derivatives of molecules;

(iii) separating the ~~up~~ 3 to 8 samples of differential labelled derivatives of molecules into fractions;

(iv) enzymatically cleaving the ~~at least three~~ 3 to 8 samples of differential labelled derivatives of molecules into fragments;

(v) separating the fragments;

(vi) examining the fragments by mass spectrometry; and

(vii) sequencing the fragments.